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NEWS	1		Web Page URLs for STN Seminar Schedule - N. America
NEWS	2	JAN 08	CHEMLIST enhanced with New Zealand Inventory of Chemicals
NEWS	3	JAN 16	CA/CAplus Company Name Thesaurus enhanced and reloaded
NEWS	4	JAN 16	IPC version 2007.01 thesaurus available on STN
NEWS	5	JAN 16	WPIDS/WPINDEX/WPIX enhanced with IPC 8 reclassification data
NEWS	6	JAN 22	CA/CAplus updated with revised CAS roles
NEWS	7	JAN 22	CA/CAplus enhanced with patent applications from India
NEWS	8	JAN 29	PHAR reloaded with new search and display fields
NEWS	9	JAN 29	CAS Registry Number crossover limit increased to 300,000 in multiple databases
NEWS	10	FEB 15	PATDPASPC enhanced with Drug Approval numbers
NEWS	11	FEB 15	RUSSIAPAT enhanced with pre-1994 records
NEWS	12	FEB 23	KOREAPAT enhanced with IPC 8 features and functionality
NEWS	13	FEB 26	MEDLINE reloaded with enhancements
NEWS	14	FEB 26	EMBASE enhanced with Clinical Trial Number field
NEWS	15	FEB 26	TOXCENTER enhanced with reloaded MEDLINE
NEWS	16	FEB 26	IFICDB/IFIPAT/IFIUDB reloaded with enhancements
NEWS	17	FEB 26	CAS Registry Number crossover limit increased from 10,000 to 300,000 in multiple databases
NEWS	18	MAR 15	WPIDS/WPIX enhanced with new FRAGHITSTR display format
NEWS	19	MAR 16	CASREACT coverage extended
NEWS	20	MAR 20	MARPAT now updated daily
NEWS	21	MAR 22	LWPI reloaded
NEWS	22	MAR 30	RDISCLOSURE reloaded with enhancements
NEWS	23	MAR 30	INPADOCDB will replace INPADOC on STN
NEWS	24	APR 02	JICST-EPLUS removed from database clusters and STN

NEWS EXPRESS	NOVEMBER 10 CURRENT WINDOWS VERSION IS V8.01c, CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP), AND CURRENT DISCOVER FILE IS DATED 25 SEPTEMBER 2006.
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
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 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

=> s (unnatural amino acid)
          5116 UNNATURAL
             1 UNNATURALS
          5116 UNNATURAL
                 (UNNATURAL OR UNNATURALS)
       1115088 AMINO
            44 AMINOS
       1115106 AMINO
                 (AMINO OR AMINOS)
       4357292 ACID
       1570511 ACIDS
       4854480 ACID
                 (ACID OR ACIDS)
L1        1084 (UNNATURAL AMINO ACID)
                 (UNNATURAL(W)AMINO(W)ACID)

=> s (non-cognate)
        869100 NON
            34 NONS
        869127 NON
                 (NON OR NONS)
         11904 COGNATE
           157 COGNATES
         12023 COGNATE
                 (COGNATE OR COGNATES)
L2         248 (NON-COGNATE)
                 (NON(W)COGNATE)

=> s alloprotein
            13 ALLOPROTEIN
            11 ALLOPROTEINS
L3          14 ALLOPROTEIN
                 (ALLOPROTEIN OR ALLOPROTEINS)
```

```
=> s L1 or L2 or L3
L4          1340 L1 OR L2 OR L3

=> s glycoprotein AND L4
          100936 GLYCOPROTEIN
          110940 GLYCOPROTEINS
          155730 GLYCOPROTEIN
                   (GLYCOPROTEIN OR GLYCOPROTEINS)
L5            18 GLYCOPROTEIN AND L4

=> s glycosyl AND L4
           11519 GLYCOSYL
              15 GLYCOSYLS
           11528 GLYCOSYL
                   (GLYCOSYL OR GLYCOSYLS)
L6             1 GLYCOSYL AND L4

=> s N-glycosylation or O-glycosylation or acetylation or acylation or
(lipid-modification) or (palmytoylation or phosphorylation
UNMATCHED LEFT PARENTHESIS 'OR (PALMYTOYLA'
The number of right parentheses in a query must be equal to the
number of left parentheses.

=> s N-glycosylation or O-glycosylation or acetylation or acylation or
(lipid-modification) or palmytoylation or phosphorylation
         3030527 N
           36299 GLYCOSYLATION
             569 GLYCOSYLATIONS
           36434 GLYCOSYLATION
                   (GLYCOSYLATION OR GLYCOSYLATIONS)
            3928 N-GLYCOSYLATION
                   (N(W)GLYCOSYLATION)
         1538815 O
           36299 GLYCOSYLATION
             569 GLYCOSYLATIONS
           36434 GLYCOSYLATION
                   (GLYCOSYLATION OR GLYCOSYLATIONS)
            1366 O-GLYCOSYLATION
                   (O(W)GLYCOSYLATION)
           69933 ACETYLATION
             268 ACETYLATIONS
           70003 ACETYLATION
                   (ACETYLATION OR ACETYLATIONS)
           59722 ACYLATION
             876 ACYLATIONS
           59978 ACYLATION
                   (ACYLATION OR ACYLATIONS)
          285507 LIPID
          210569 LIPIDS
          350719 LIPID
                   (LIPID OR LIPIDS)
          295920 MODIFICATION
          119269 MODIFICATIONS
          395180 MODIFICATION
                   (MODIFICATION OR MODIFICATIONS)
             678 LIPID-MODIFICATION
                   (LIPID(W)MODIFICATION)
               0 PALMYTOYLATION
          163534 PHOSPHORYLATION
            1774 PHOSPHORYLATIONS
          163812 PHOSPHORYLATION
                   (PHOSPHORYLATION OR PHOSPHORYLATIONS)
```

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L7      290927 N-GLYCOSYLATION OR O-GLYCOSYLATION OR ACETYLATION OR ACYLATION
               OR (LIPID-MODIFICATION) OR PALMYTOYLATION OR PHOSPHORYLATION

=> s L4 AND L7
L8          55 L4 AND L7

=> s L8 or l5 or l6
L9          73 L8 OR L5 OR L6

=> s L9 and translation
        534906 TRANSLATION
          1975 TRANSLATIONS
        536435 TRANSLATION
                 (TRANSLATION OR TRANSLATIONS)
L10          9 L9 AND TRANSLATION

=> s L9 and protein
       1997460 PROTEIN
       1396814 PROTEINS
       2324845 PROTEIN
                 (PROTEIN OR PROTEINS)
L11         39 L9 AND PROTEIN

=> d ti,so,ibib,abs 1-15 L11

L11  ANSWER 1 OF 39  HCAPLUS  COPYRIGHT 2007 ACS on STN
TI   Site specific fluorinated unnatural amino
     acids in proteins probed by 19F NMR as a tool for
     probing protein conformational changes
SO   Abstracts of Papers, 233rd ACS National Meeting, Chicago, IL, United
     States, March 25-29, 2007 (2007), CHED-954 Publisher: American Chemical
     Society, Washington, D. C.
     CODEN: 69JAUY
ACCESSION NUMBER:        2007:291331  HCAPLUS
TITLE:                   Site specific fluorinated unnatural
                         amino acids in proteins
                         probed by 19F NMR as a tool for probing
                         protein conformational changes
AUTHOR(S):               Mehl, Ryan A.; Hammill, Jared T.
CORPORATE SOURCE:        Department of Chemistry, Franklin & Marshall College,
                         Lancaster, PA, 17604-3003, USA
SOURCE:                  Abstracts of Papers, 233rd ACS National Meeting,
                         Chicago, IL, United States, March 25-29, 2007 (2007),
                         CHED-954.  American Chemical Society: Washington, D.
                         C.
                         CODEN: 69JAUY
DOCUMENT TYPE:           Conference; Meeting Abstract; (computer optical disk)
LANGUAGE:                English
AB   Site-specific incorporation of fluorinated amino acids using altered
     translational machinery provides access to detailed studies on
     protein conformational changes.  Nitrogen Regulatory
     Protein C (NtrC), a pos. acting bacterial transcription factor,
     makes up one unit of a two component regulatory system.  The other unit, a
     sensor histidine kinase, phosphorylates the D54 residue in the amino
     (N)-terminal domain of NtrC in response to changes in nitrogen concentration
The
     receiver domain of NtrC is thus activated by phosphorylation and
     sends a signal to the NtrC transcriptional activator domain via structural
     rearrangements.  In this study, para-trifluoromethylphenylalanine (TFM)
     was introduced site-specifically into NtrC, in vivo, with an altered
     tRNA/aminoacyl-tRNA synthetase pair.  TFM was site-specifically inserted
     in response to the TAG nonsense codon at sites 5, 66, 94, 99, and 101 to
     produce NtrC variants that could be monitored by 19F NMR.  By monitoring
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the chemical shifts of the 19F signal from labeled NtrC variants the conformational changes/structural rearrangements taking place in response to varying levels of nitrogen can be investigated.

L11 ANSWER 2 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN
TI Semisynthesis of unnatural amino acid mutants of paxillin: protein probes for cell migration studies
SO Protein Science (2007), 16(3), 550-556
CODEN: PRCIEI; ISSN: 0961-8368
ACCESSION NUMBER: 2007:262951 HCAPLUS
TITLE: Semisynthesis of unnatural amino acid mutants of paxillin: protein probes for cell migration studies
AUTHOR(S): Vogel, Elizabeth M.; Imperiali, Barbara
CORPORATE SOURCE: Department of Chemistry, Massachusetts Institute of Technology, Cambridge, MA, 02139, USA
SOURCE: Protein Science (2007), 16(3), 550-556
CODEN: PRCIEI; ISSN: 0961-8368
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Caged phosphopeptides and phosphoproteins are valuable tools for dissecting the dynamic role of phosphorylation in complex signaling networks with temporal and spatial control. Demonstrating the broad scope of phosphoamino acid caging for studying signaling events, the authors report here the semisynthesis of a photolabile precursor to the cellular migration protein paxillin, which is a complex, multidomain phosphoprotein. This semisynthetic construct provides a powerful probe for investigating the influence that phosphorylation of paxillin at a single site has on cellular migration. The 61-kDa paxillin construct was assembled using native chemical ligation to install a caged phosphotyrosine residue at position 31 of the 557-residue protein, and the probe includes all other binding and localization determinants in the paxillin macromol., which are essential for creating a native environment to investigate phosphorylation. Following semisynthesis, paxillin variants were characterized through detailed biochem. analyses and by quant. uncaging studies.
REFERENCE COUNT: 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN
TI Lysine Nζ-Decarboxylation in the BlaR1 Protein from Staphylococcus aureus at the Root of Its Function As an Antibiotic Sensor
SO Journal of the American Chemical Society (2007), 129(13), 3834-3835
CODEN: JACSAT; ISSN: 0002-7863
ACCESSION NUMBER: 2007:253144 HCAPLUS
TITLE: Lysine Nζ-Decarboxylation in the BlaR1 Protein from Staphylococcus aureus at the Root of Its Function As an Antibiotic Sensor
AUTHOR(S): Cha, Jooyoung; Mobashery, Shahriar
CORPORATE SOURCE: Department of Chemistry and Biochemistry, University of Notre Dame, Notre Dame, IN, 46556, USA
SOURCE: Journal of the American Chemical Society (2007), 129(13), 3834-3835
CODEN: JACSAT; ISSN: 0002-7863
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The structure of the surface domain of the BlaR1 protein of Staphylococcus aureus, a β-lactam antibiotic sensor/signal transducer, is essentially identical to that of the class D β-lactamases, which are antibiotic resistance enzymes. Both

proteins have an unusual N-carboxylated lysine within their active sites, which promotes a serine for acylation by the antibiotic. N-Carboxylated lysine also catalyzes hydrolytic deacylation of the acyl-enzyme species in the β-lactamase. The situation with the BlaR1 protein is different in that on acylation of serine N-carboxylated lysine experiences decarboxylation, whereby the process is arrested in the acyl-protein stage. As such, BlaR1 experience acylation by the antibiotic that it senses, an event that enjoys longevity for at least the duration of one bacterial generation. We report herein the production of S-(4-butanoate)-cysteine, as a surrogate of N-carboxylated lysine at position 392 of the BlaR1 protein. This unnatural amino acid cannot experience N-decarboxylation. We observed that BlaR1 protein modified at position 392 by S-(4-butanoate)-cysteine behaves as a reasonable β-lactamase. We have shown herein that the mechanistic basis for the BlaR1 protein serving as a receptor is solely its ability to undergo N-decarboxylation of the active site lysine on protein acylation by its antibiotic ligand.

REFERENCE COUNT: 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 4 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Modification of Aniline Containing Proteins Using an Oxidative Coupling Strategy

SO Journal of the American Chemical Society (2006), 128(49), 15558-15559 CODEN: JACSAT; ISSN: 0002-7863

ACCESSION NUMBER: 2006:1193539 HCAPLUS

DOCUMENT NUMBER: 146:138111

TITLE: Modification of Aniline Containing Proteins Using an Oxidative Coupling Strategy

AUTHOR(S): Hooker, Jacob M.; Esser-Kahn, Aaron P.; Francis, Matthew B.

CORPORATE SOURCE: Department of Chemistry, University of California, Berkeley, CA, 94720-1460, USA

SOURCE: Journal of the American Chemical Society (2006), 128(49), 15558-15559 CODEN: JACSAT; ISSN: 0002-7863

PUBLISHER: American Chemical Society

DOCUMENT TYPE: Journal

LANGUAGE: English

AB A new bioconjugation reaction has been developed based on the chemoselective modification of anilines through an oxidative coupling pathway. Aryl amines were installed on the surface of protein substrates through lysine acylation reactions or through the use of native chemical ligation techniques. Upon exposure to NaIO4 in aqueous buffer, the anilines coupled rapidly to the aromatic rings of N,N-dialkyl-N'-acyl-p-phenylenediamines. The identities of the reaction products were confirmed using ESI-MS and through comparison to small mol. analogs. Control expts. indicated that none of the native amino acids participated in the reaction. The resulting bioconjugates were found to be stable toward hydrolysis from pH 4 to pH 11 and in the presence of many commonly used oxidants, reductants, and nucleophiles. A fluorescent phenylenediamine reagent was synthesized for the selective detection of aniline labeled proteins in mixts., and the reaction was used to append the C-terminus of the green fluorescent protein with a single PEG chain. When combined with techniques for the incorporation of unnatural amino acids into proteins, this bioorthogonal coupling method should prove useful for a number of applications requiring a high degree of labeling specificity.

REFERENCE COUNT: 35 THERE ARE 35 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 5 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Global incorporation of unnatural amino acids in Escherichia coli
SO Methods in Molecular Biology (Totowa, NJ, United States) (2007), 352(Protein Engineering Protocols), 23-34
CODEN: MMBIED; ISSN: 1064-3745

ACCESSION NUMBER: 2006:1174695 HCAPLUS
DOCUMENT NUMBER: 146:269552
TITLE: Global incorporation of unnatural amino acids in Escherichia coli
AUTHOR(S): Bacher, Jamie M.; Ellington, Andrew D.
CORPORATE SOURCE: The Skaggs Institute for Chemical Biology, The Scripps Research Institute, La Jolla, CA, USA
SOURCE: Methods in Molecular Biology (Totowa, NJ, United States) (2007), 352(Protein Engineering Protocols), 23-34
CODEN: MMBIED; ISSN: 1064-3745
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The incorporation of amino acid analogs is becoming increasingly useful. Site-specific incorporation of unnatural amino acids allows the application of chemical biol. to protein -specific investigations and applications. However, the global incorporation of unnatural amino acids allows for tests of proteomic and genetic code hypotheses. For example, the adaptation of organisms to unnatural amino acids may lead to new genetic codes. To understand and quantify changes from such perturbations, an understanding is required of the microbiol. and proteomic responses to the incorporation of unnatural amino acids. Here we describe protocols to characterize the effects of such proteome-wide perturbations.

REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 6 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN
TI Semisynthetic proteins in mechanistic studies: using chemistry to go where nature can't
SO Current Opinion in Chemical Biology (2006), 10(5), 487-491
CODEN: COCBF4; ISSN: 1367-5931

ACCESSION NUMBER: 2006:967685 HCAPLUS
DOCUMENT NUMBER: 146:2131
TITLE: Semisynthetic proteins in mechanistic studies: using chemistry to go where nature can't
AUTHOR(S): Pellois, Jean-Philippe; Muir, Tom W.
CORPORATE SOURCE: The Laboratory of Synthetic Protein Chemistry, The Rockefeller University, New York, NY, 10021, USA
SOURCE: Current Opinion in Chemical Biology (2006), 10(5), 487-491
CODEN: COCBF4; ISSN: 1367-5931
PUBLISHER: Elsevier B.V.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. The manipulation of the chemical structure of proteins beyond what is feasible with standard genetics, offers a powerful strategy to investigate protein mechanisms. By allowing the incorporation of biophys. probes, unnatural amino acids, and post-translational modifications in proteins, chemical-driven approaches have greatly contributed to the understanding of the mol. basis of protein function.

REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 7 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI tRNAHis guanylyltransferase adds G-1 to the 5' end of tRNAHis by recognition of the anticodon, one of several features unexpectedly shared with tRNA synthetases
SO RNA (2006), 12(6), 1007-1014
CODEN: RNARFU; ISSN: 1355-8382

ACCESSION NUMBER: 2006:545655 HCAPLUS
DOCUMENT NUMBER: 145:467203
TITLE: tRNAHis guanylyltransferase adds G-1 to the 5' end of tRNAHis by recognition of the anticodon, one of several features unexpectedly shared with tRNA synthetases
AUTHOR(S): Jackman, Jane E.; Phizicky, Eric M.
CORPORATE SOURCE: Department of Biochemistry and Biophysics, University of Rochester School of Medicine, Rochester, NY, 14642, USA
SOURCE: RNA (2006), 12(6), 1007-1014
CODEN: RNARFU; ISSN: 1355-8382
PUBLISHER: Cold Spring Harbor Laboratory Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB All eukaryotic tRNAHis mols. are unique among tRNA species because they require addition of a guanine nucleotide at the -1 position by tRNAHis guanylyltransferase, encoded in yeast by THG1. This G-1 residue is both necessary and sufficient for aminoacylation of tRNA by histidyl-rRNA synthetase in vitro and is required for aminoacylation in vivo. Although Thg1 is presumed to be highly specific for tRNAHis to prevent mis-acylation of tRNAs, the source of this specificity is unknown. We show here that Thg1 is >10,000-fold more selective for its cognate substrate tRNAHis than for the non-cognate substrate tRNAPhe. We also demonstrate that the GUG anticodon of tRNAHis is a crucial Thg1 identity element, since alteration of this anticodon in tRNAHis completely abrogates Thg1 activity, and the simple introduction of this GUG anticodon to any of three non-cognate tRNAs results in significant Thg1 activity. For tRNAPhe, kcat/KM is improved by at least 200-fold. Thg1 is the only protein other than aminoacyl-tRNA synthetases that is known to use the anticodon as an identity element to discriminate among tRNA species while acting at a remote site on the tRNA, an unexpected link given the lack of any identifiable sequence similarity between these two families of proteins. Moreover, Thg1 and tRNA synthetases share two other features: they act in close proximity to one another at the top of the tRNA aminoacyl-acceptor stem, and the chemical of their resp. reactions is strikingly similar.

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 8 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN
TI Misacylation of tRNA in prokaryotes: a re-evaluation
SO Cellular and Molecular Life Sciences (2006), 63(7-8), 820-831
CODEN: CMLSFI; ISSN: 1420-682X

ACCESSION NUMBER: 2006:491135 HCAPLUS
DOCUMENT NUMBER: 145:204557
TITLE: Misacylation of tRNA in prokaryotes: a re-evaluation
AUTHOR(S): Stortchevoi, A. A.
CORPORATE SOURCE: Yale University School of Medicine, Yale University, New Haven, CT, 06510, USA
SOURCE: Cellular and Molecular Life Sciences (2006), 63(7-8), 820-831
CODEN: CMLSFI; ISSN: 1420-682X
PUBLISHER: Birkhaeuser Verlag
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review. Misacylation of tRNA by a non-cognate amino

acid is a natural phenomenon and occurs with a frequency of approx. 1 in 10,000 due to occasional mistakes in aminoacyl tRNA synthesis. In a number of prokaryotic organisms, misacylation of selenocysteinyl tRNA, glutaminyl tRNA and aspartyl tRNAs has particular physiol. meaning. Recently, misacylation has emerged as a powerful tool for studying specific interactions between aa-tRNAs and associated protein factors. The present review provides an overview of the application of misacylated tRNA in research.

REFERENCE COUNT: 121 THERE ARE 121 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 9 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Interactions between the YycFG and PhoPR two-component systems in Bacillus subtilis: the PhoR kinase phosphorylates the non-cognate YycF response regulator upon phosphate limitation. [Erratum to document cited in CA144:386073]

SO Molecular Microbiology (2006), 60(2), 535
CODEN: MOMIEE; ISSN: 0950-382X

ACCESSION NUMBER: 2006:449125 HCAPLUS
DOCUMENT NUMBER: 144:447733
TITLE: Interactions between the YycFG and PhoPR two-component systems in Bacillus subtilis: the PhoR kinase phosphorylates the non-cognate YycF response regulator upon phosphate limitation. [Erratum to document cited in CA144:386073]
AUTHOR(S): Howell, Alistair; Dubrac, Sarah; Noone, David; Varughese, Kottayil I.; Devine, Kevin
CORPORATE SOURCE: Department of Genetics, Smurfit Institute, Trinity College Dublin, Dublin, 2, Ire.
SOURCE: Molecular Microbiology (2006), 60(2), 535
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Publishing Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB In Discussion, page 12, line 40, the word "promoters" should be replaced with "protomers". The correct sentence should read: "The phosphotransferase domain of histidine kinases are four-helix bundles formed through the dimerization of two helical hairpin structures from the two protomers that make up a kinase dimer (Fig. 10).".

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 10 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Use of stop codons and their suppressor tRNAs charged with N-acetylgalactosaminides of amino acids to incorporate glycosidation sites in proteins manufactured in Eubacteria

SO PCT Int. Appl., 119 pp.
CODEN: PIXXD2

ACCESSION NUMBER: 2006:383474 HCAPLUS
DOCUMENT NUMBER: 144:426803
TITLE: Use of stop codons and their suppressor tRNAs charged with N-acetylgalactosaminides of amino acids to incorporate glycosidation sites in proteins manufactured in Eubacteria
INVENTOR(S): Schultz, Peter G.; Hanson, Sarah R.; Xu, Ran; Zhang, Zhiwen; Wong, Chi-Huey
PATENT ASSIGNEE(S): The Scripps Research Institute, USA
SOURCE: PCT Int. Appl., 119 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2006045116	A2	20060427	WO 2005-US38250	20051020
WO 2006045116	A3	20061228		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

US 2006110796	A1	20060525	US 2005-255601	20051020
PRIORITY APPLN. INFO.:			US 2004-620898P	P 20041020

AB Methods of incorporating amino acids containing N-acetylgalactosamine into proteins at translation are described. The glycosidated amino acids can be used as the starting point for further glycosidation and so allow the development of mammalian glycosidation patterns in proteins manufactured in Eubacterial hosts. This may be achieved using an aminoacyl tRNA synthetase with relaxed substrate requirements to charge its cognate tRNA with an N-acetylgalactosamine-containing unnatural amino acid. Variants of the tyrosyl tRNA synthetase of Methanococcus jannaschii capable of accepting N-acetylgalactosaminides of threonine or serine as substrates were developed by directed evolution. The tRNAs used were tyrosine amber suppressor tyrosine tRNAs. Use of the enzyme and tRNAs to glycosidate myoglobin encoded by a gene containing an amber mutation in an Escherichia coli expression host is demonstrated.

L11 ANSWER 11 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Interactions between the YycFG and PhoPR two-component systems in Bacillus subtilis: the PhoR kinase phosphorylates the non-cognate YycF response regulator upon phosphate limitation

SO Molecular Microbiology (2006), 59(4), 1199-1215
CODEN: MOMIEE; ISSN: 0950-382X

ACCESSION NUMBER: 2006:271206 HCAPLUS
DOCUMENT NUMBER: 144:386073

TITLE: Interactions between the YycFG and PhoPR two-component systems in Bacillus subtilis: the PhoR kinase phosphorylates the non-cognate YycF response regulator upon phosphate limitation

AUTHOR(S): Howell, Alistair; Dubrac, Sarah; Noone, David; Varughese, Kottayil I.; Devine, Kevin

CORPORATE SOURCE: Department of Genetics, Smurfit Institute, Trinity College Dublin, Dublin, 2, Ire.

SOURCE: Molecular Microbiology (2006), 59(4), 1199-1215
CODEN: MOMIEE; ISSN: 0950-382X

PUBLISHER: Blackwell Publishing Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two-component signal transduction systems (TCS) are an important mechanism by which bacteria sense and respond to their environment. Although each two-component system appears to detect and respond to a specific signal(s), it is now evident that they do not always act independently of each other. In this paper we present data indicating regulatory links between the PhoPR two-component system that participates in the cellular response to phosphate limitation, and the essential YycFG two-component system in Bacillus subtilis. We show that the PhoR sensor kinase can

activate the YycF response regulator during a phosphate limitation-induced stationary phase, and that this reaction occurs in the presence of the cognate YycG sensor kinase. Phosphorylation of YycF by PhoR also occurs in vitro, albeit at a reduced level. However, the reciprocal cross-phosphorylation does not occur. A second level of interaction between PhoPR and YycFG is indicated by the fact that cells depleted for YycFG have a severely deficient PhoPR-dependent phosphate limitation response and that YycF can bind directly to the promoter of the phoPR operon. YycFG-depleted cells neither activate expression of phoA and phoPR nor repress expression of the essential tagAB and tagDEF operons upon phosphate limitation. This effect is specific to the PhoPR-dependent phosphate limitation response because PhoPR-independent phosphate limitation responses can be initiated in YycFG-depleted cells.

REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 12 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Possibility of application of sugar chain modification technology to drug development

SO Farumashia (2005), 41(4), 325-330
CODEN: FARUAW; ISSN: 0014-8601

ACCESSION NUMBER: 2005:338889 HCAPLUS
DOCUMENT NUMBER: 142:406809
TITLE: Possibility of application of sugar chain modification technology to drug development
AUTHOR(S): Nishimura, Shin-Ichiro
CORPORATE SOURCE: Grad. Sch. Sci., Hokkaido Univ., Japan
SOURCE: Farumashia (2005), 41(4), 325-330
CODEN: FARUAW; ISSN: 0014-8601
PUBLISHER: Pharmaceutical Society of Japan
DOCUMENT TYPE: Journal; General Review
LANGUAGE: Japanese

AB A review on the development of NESP (novel erythropoiesis-stimulating protein; hyperglycosylated analog of human erythropoietin), site-specific introduction of sialyloligosaccharides into insulin for prolongation of biol. activity, preparation of cyclic glycopeptides as influenza virus hemagglutinin blockers, preparation of unnatural amino acid tRNAs, and synthesis of selectively glycosylated proteins.

L11 ANSWER 13 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Functional characterization in vitro of all two-component signal transduction systems from Escherichia coli

SO Journal of Biological Chemistry (2005), 280(2), 1448-1456
CODEN: JBCHA3; ISSN: 0021-9258

ACCESSION NUMBER: 2005:21474 HCAPLUS
DOCUMENT NUMBER: 142:276561
TITLE: Functional characterization in vitro of all two-component signal transduction systems from Escherichia coli
AUTHOR(S): Yamamoto, Kaneyoshi; Hirao, Kiyo; Oshima, Taku; Aiba, Hirofumi; Utsumi, Ryutaro; Ishihama, Akira
CORPORATE SOURCE: Department of Agricultural Chemistry, Kinki University, Nara, 631-8505, Japan
SOURCE: Journal of Biological Chemistry (2005), 280(2), 1448-1456
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Bacteria possess a signal transduction system, referred to as a 2-component system, for adaptation to external stimuli. Each 2-component

system consists of a sensor protein-histidine kinase (HK) and a response regulator (RR), together forming a signal transduction pathway via histidyl-aspartyl phospho-relay. A total of 30 sensor HKs, including as yet uncharacterized putative HKs (BaeS, BasS, CreC, CusS, HydH, RstB, YedV, and YfhK), and a total of 34 RRs, including putative RRs (BaeR, BasR, CreB, CusR, HydG, RstA, YedW, YfhA, YgeK, and YhjB), have been suggested to exist in E. coli. We have purified the carboxyl-terminal catalytic domain of 27 sensor HKs and the full-length protein of all 34 RRs to apparent homogeneity. Self-phosphorylation in vitro was detected for 25 HKs. The rate of self-phosphorylation differed among HKs, whereas the level of phosphorylation was generally co-related with the phosphorylation rate. However, the phosphorylation level was low for ArcB, HydH, NarQ, and NtrB even though the reaction rate was fast, whereas the level was high for the slow phosphorylation species BasS, CheA, and CreC. By using the phosphorylated HKs, we examined trans-phosphorylation in vitro of RRs for all possible combinations. Trans-phosphorylation of presumed cognate RRs by HKs was detected, for the 1st time, for 8 pairs, BaeS-BaeR, BasS-BasR, CreC-CreB, CusS-CusR, HydH-HydG, RstB-RstA, YedV-YedW, and YfhK-YfhA. All trans-phosphorylation took place within less than 1/2 min, but the stability of phosphorylated RRs differed, indicating the involvement of de-phosphorylation control. In addition to the trans-phosphorylation between the cognate pairs, we detected trans-phosphorylation between about 3% of non-cognate HK-RR pairs, raising the possibility that the cross-talk in signal transduction takes place between 2-component systems.

REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 14 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Expanding the eukaryotic genetic code using orthologous aminoacyl-tRNA synthetases genetically engineered for specificity toward non-natural amino acids

SO PCT Int. Appl., 276 pp.
CODEN: PIXXD2

ACCESSION NUMBER: 2004:934465 HCAPLUS
DOCUMENT NUMBER: 141:389844
TITLE: Expanding the eukaryotic genetic code using orthologous aminoacyl-tRNA synthetases genetically engineered for specificity toward non-natural amino acids
INVENTOR(S): Chin, Jason W.; Cropp, Ashton T.; Anderson, Christopher J.; Schultz, Peter G.
PATENT ASSIGNEE(S): The Scripps Research Institute, USA
SOURCE: PCT Int. Appl., 276 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2004094593	A2	20041104	WO 2004-US11786	20040416

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE,

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AU 2004233083	A1	20041104	AU 2004-233083	20040416
CA 2520750	A1	20041104	CA 2004-2520750	20040416
US 2004265952	A1	20041230	US 2004-826919	20040416
AU 2004253857	A1	20050113	AU 2004-253857	20040416
CA 2527877	A1	20050113	CA 2004-2527877	20040416
US 2005009049	A1	20050113	US 2004-825867	20040416
WO 2005003294	A2	20050113	WO 2004-US11833	20040416

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RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP 1613735	A2	20060111	EP 2004-759917	20040416

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EP 1636340	A2	20060322	EP 2004-785787	20040416

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BR 2004011475	A	20060725	BR 2004-11475	20040416
US 2006246509	A1	20061102	US 2006-561121	20060523

PRIORITY APPLN. INFO.:	US 2003-463869P	P 20030417
	US 2003-479931P	P 20030618
	US 2003-493014P	P 20030805
	US 2003-496548P	P 20030819
	WO 2004-US11786	W 20040416
	WO 2004-US11833	W 20040416

AB This invention provides compns. and methods for producing translational components that expand the number of genetically encoded amino acids in eukaryotic cells. The components include orthogonal tRNAs, orthogonal aminoacyl-tRNA synthetases, orthogonal pairs of tRNAs/synthetases, and unnatural amino acids. Thus, Escherichia coli tyrosyl-tRNA synthetase (EcTyrRS) forms an orthogonal pair with the Bacillus stearothermophilus tRNACUA in mammalian cells. A general approach for the isolation of aminoacyl-tRNA synthetases that incorporate unnatural amino acids with high fidelity into proteins in response to an amber codon in Saccharomyces cerevisiae is based on the activation of GAL4 responsive reporter genes (HIS3, URA3, or LacZ) by suppression of amber codons between the DNA-binding domain and transcriptional activation domain of GAL4. The optimization of a GAL4 reporter for pos. selection of active EcTyrRS variants is described. A neg. selection of inactive EcTyrRS variants is also developed with the URA3 reporter by use of a small mol. (5-fluoroorotic acid) added to the growth media as a 'toxic allele'. Five amino acids have been incorporated into proteins efficiently, with high fidelity, in response to the nonsense codon TAG in S. cerevisiae: p-acetyl-L-phenylalanine, p-benzoyl-L-phenylalanine, p-azido-L-phenylalanine, O-methyl-L-tyrosine, and p-iodo-L-phenylalanine. A highly efficient method for the selective modification of proteins is described, which involves the genetic incorporation of azide or acetylene containing unnatural amino acids into protein in response to the amber nonsense codon; these amino acid side chains can then be modified by a Huisgen [3+2] cycloaddn. reaction.

L11 ANSWER 15 OF 39 HCAPLUS COPYRIGHT 2007 ACS on STN

TI Transfer RNA-dependent amino acid discrimination by aminoacyl-tRNA synthetases
SO Translation Mechanisms (2003), 34-64. Editor(s): Lapointe, Jacques; Brakier-Gingras, Lea. Publisher: Landes Bioscience, Georgetown, Tex. CODEN: 69FYBX; ISBN: 0-306-47839-0

ACCESSION NUMBER: 2004:841422 HCAPLUS
DOCUMENT NUMBER: 142:387968
TITLE: Transfer RNA-dependent amino acid discrimination by aminoacyl-tRNA synthetases
AUTHOR(S): Hendrickson, Tamara L.; Schimmel, Paul
CORPORATE SOURCE: Department of Chemistry, Johns Hopkins University, Baltimore, MD, USA
SOURCE: Translation Mechanisms (2003), 34-64. Editor(s): Lapointe, Jacques; Brakier-Gingras, Lea. Landes Bioscience: Georgetown, Tex.
CODEN: 69FYBX; ISBN: 0-306-47839-0
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review. Aminoacyl-tRNA synthetases (AARSs) form a direct connection between the trinucleotide codons of the genetic code and their corresponding amino acids (AA). Each AARS catalyzes the biosynthesis of a specific, cognate set of AA-tRNAAA isoacceptors. In some cases, the cognate amino acid is structurally similar to one or more encoded amino acids and/or other available metabolites, leading to mis-activation and mis-acylation of non-cognate amino acids.
To remedy these errors, many AARSs have tRNA-dependent hydrolytic editing activities against mis-activated, non-cognate amino acids. In this manner, the accuracy of translation is maintained at a level that is higher than could be achieved by simple, one-step, side chain recognition. A resurgence in interest in tRNA-dependent editing mechanisms has occurred over the past decade. Proofreading mechanisms have now been identified in as many as nine different AARSs. Here, the role of tRNA-dependent editing in guaranteeing the accuracy of tRNA aminoacylation is summarized.

REFERENCE COUNT: 127 THERE ARE 127 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

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L12 39 DUP REM L11 (0 DUPLICATES REMOVED)